

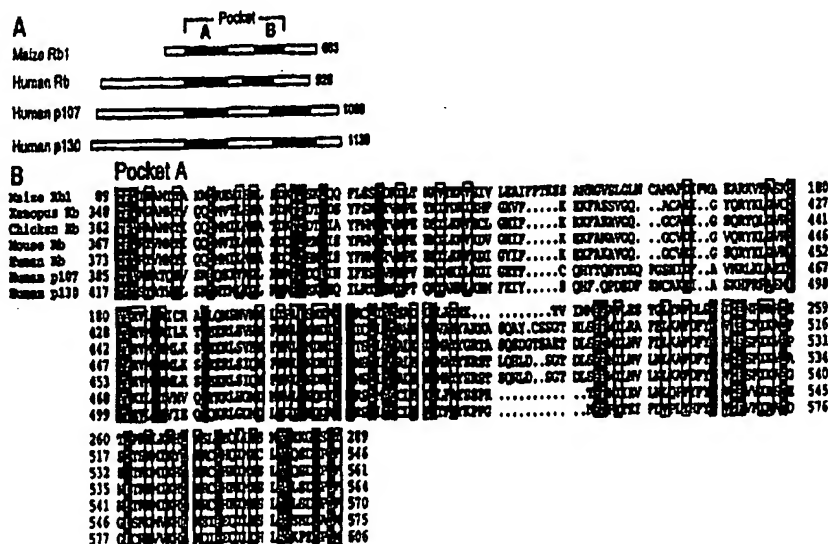


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(54) Title: PLANT RETINOBLASTOMA-ASSOCIATED PROTEINS



(57) Abstract

The present invention is based on the isolation and characterization of a plant cell DNA sequence encoding for a retinoblastoma protein. Such finding is based on the structural and functional properties of the plant retinoblastoma protein as possible regulator of the cellular cycle, of the cellular growth and of the plant cellular differentiation. For this reason, among other aspects, it is claimed the use of retinoblastoma protein or the DNA sequence which encodes for it in the growing control of vegetable cells, plants and/or vegetable virus, as well as the use of vectors, cells, plants or animals, or animal cells modified through the manipulation of the control route based on plant retinoblastoma protein.

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PLANT RETINOBLASTOMA-ASSOCIATED PROTEINS**DESCRIPTION**

The present invention relates the proteins having biological activity in plant and animal systems, to polynucleotides encoding for the expression of such proteins, to oligonucleotides for use in identifying and synthesizing these proteins and polynucleotides, to vectors and cells containing the polynucleotides in recombinant form and to plants and animals comprising these, and to the use of the proteins and polynucleotides and fragments thereof in the control of plant growth and plant vulnerability to viruses.

Cell cycle progression is regulated by positive and negative effectors. Among the latter, the product of the retinoblastoma susceptibility gene (Rb) controls the passage of mammalian cells through G1 phase. In mammalian cells, Rb regulates G1/S transit by inhibiting the function of the E2F family of transcription factors, known to interact with sequences in the promoter region of genes required for cellular DNA replication (see eg Weinberg, R.A. Cell 81,323 (1995); Nevins, J.R. Science 258,424 (1992)). DNA tumor viruses that infect animal cells express oncoproteins that interact with the Rb protein via a LXCXE motif, disrupting Rb-E2F complexes and driving cells into S-phase (Weinberg *ibid*; Ludlow, J. W. FASEB J. 7, 866 (1993); Moran, E. FASEB J. 7, 880 (1993); Vousden, K. FASEB J. 7, 872 (1993)).

The present inventors have shown that efficient replication of a plant geminivirus requires the integrity of an LXCXE amino acid motif in the viral RepA protein and that RepA can interact with members of the human Rb family in yeast (Xie, Q., Suárez-López, P. and Gutiérrez, C. EMBO J. 14, 4073 (1995). The presence of the LXCXE motif in plant D-type cyclins has also been reported (Soni, R., Carmichael, J. P., Shah, Z. H. and Murray, J.

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A. H. Plant Cell 7, 85-103 (1995)).

The present inventors have now identified characteristic sequences of plant Rb proteins and corresponding encoding polynucleotides for the first time, isolated such a protein and polynucleotide, and particularly have identified sequences that distinguish it from known animal Rb protein sequences. The inventors have determined that a known DNA sequence from the maize encoding a vegetable Rb plant protein and is hereinafter called ZmRb1. ZmRb1 has been demonstrated by the inventors to interact in yeasts with RepA, a plant geminivirus protein containing LXCXE motif essential for its function. The inventors have further determined that geminivirus DNA replication is reduced in plant cells transfected with plasmids encoding either ZmRb1 or human p130, a member of the human Rb family.

Significantly the inventors work suggests that plant and animal cells may share fundamentally similar strategies for growth control, and thus human as well as plant Rb protein such as ZmRb1 will be expected to have utility in, *inter alia*, plant therapeutics, diagnostics, growth control or investigations and many such plant proteins will have similar utility in animals.

In a first aspect of the present invention there is provided the use of retinoblastoma protein in controlling the growth of plant cells and/or plant viruses. Particularly, the present invention provides control of viral infection and/or growth in plant cells wherein the virus requires the integrity of an LXCXE amino acid motif in one of its proteins, particularly, e. g., in the viral RepA protein, for normal reproduction. Particular plant viruses so controlled are Geminiviruses.

A preferred method of control using such proteins involves applying these to the plant cell, either directly or by introduction of DNA or RNA encoding for

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their expression into the plant cell which it is desired to treat. By over expressing the retinoblastoma protein, or expressing an Rb protein or peptide fragment thereof that interacts with the LXCXE motif of the virus but does not affect the normal functioning of the cell, it is possible to inhibit normal virus growth and thus also to produce infection spreading from that cell to its neighbours.

Alternatively, by means of introducing anti-sense DNA or RNA in plant cells in vectors form that contain the necessary promoters for the DNA or RNA transcription, it will be possible to exploit the well known anti-sense mechanism in order to inhibit the expression of the Rb protein, and thus the S-phase. Such plants will be of use, among other aspects to replicate DNA or RNA until high levels, e.g. in yeasts. The methods to introduce anti-sense DNA in cells are very well known for those skilled in the art: see for example "Principles of gene manipulation - An introduction to Genetic Engineering (1994) R.W. Old & S.B. Primrose; Oxford-Blackwell Scientific Publications Fifth Edition p398.

In a second aspect of the present invention there is provided recombinant nucleic acid, particularly in the form of DNA or cRNA (mRNA), encoding for expression of Rb protein that is characteristic of plants. This nucleic acid is characterised by one or more characteristic regions that differ from known animal Rb protein nucleic acid and is exemplified herein by SEQ ID No 1, bases 31-2079.

The DNA or RNA can have a sequence that contains the degenerated substitution in the nucleotides of the codons in SEQ ID No. 1, and in where the RNA the T is U. The most preferred DNA or RNA are capable of hybridate with the polynucleotide of the SEQ ID No. 1 in conditions of low stringency, preferably being the hybridization

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produced in conditions of high stringency.

The expressions "conditions of low stringency" and "conditions of high stringency" are understood by those skilled, but are conveniently exemplified in US 5202257, Col-9-Col 10. If some modifications were made to lead to the expression of a protein with different amino acids, preferably of the same kind of the corresponding amino acids to the SEQ ID No 1; that is, are conservative substitutions. Such substitutions are known by those skilled, for example, see US 5380712, and it is only contemplated when the protein has activity with retinoblastoma protein.

Preferred DNA or cRNA encodes for a plant Rb protein having A and B pocket sub-domains having between 30% and 75% homology with human Rb protein, particularly as compared with p130, more preferably from 50% to 64% homology. Particularly the plant Rb protein so encoded has the C706 amino acid of human Rb conserved. Preferably the spacer sequence between the A and B pockets is not conserved with respect to animal Rb proteins, preferably being less than 50% homologous to the same region as found in such animal proteins. Most preferably the protein so encoded has 80% or more homology with that of SEQ NO 2 of the sequence listing attached hereto, still more preferably 90% or more and most preferably 95% or more. Particularly provided is recombinant DNA of SEQ ID No 1 bases 31 to 2079, or the entire SEQ ID No 1, or corresponding RNAs, encoding for maize cDNA clone encoding ZmRb1 of SQ ID No 2.

In a third aspect of the present invention there is provided the protein expressed by the recombinant DNA or RNA of the second aspect, novel proteins derived from such DNA or RNA, and protein derived from naturally occurring DNA or RNA by mutagenic means such as use of mutagenic PCR primers.

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In a fourth aspect there are provided vectors, cells and plants and animals comprising the recombinant DNA or RNA of correct sense or anti-sense, of the invention.

5 In a particularly preferred use of the first aspect there is provided a method of controlling cell or viral growth comprising administering the DNA, RNA or protein of the second or third aspects to the cell. Such administration may be direct in the case of proteins or may involve indirect means, such as electroporation of
10 plant seed cells with DNA or by transformation of cells with expression vectors capable of expressing or over expressing the proteins of the invention or fragments thereof that are capable of inhibiting cell or viral growth.

15 Alternatively, the method uses an expression vector capable of producing anti-sense RNA of the cDNA of the invention.

Another one of the specific characteristics of the plants protein and of the nucleic acids includes a N-
20 terminal domain corresponding in sequence to the amino acids 1 to 90 of the SEQ ID No. 2 and a nucleotides sequence corresponding to the basis 31 to 300 of the SEQ ID No. 1. These sequences are characterized by possessing less than 150 and less than 450 units that the animal
25 sequences which possess more than 300 amino acids and 900 pairs of more bases.

The present invention will now be illustrated further by reference to the following non-limiting Examples. Further embodiments falling within the scope of the
30 claims attached hereto will occur to those skilled in the light of these.

Figures.

Fig. 1. The sub-figure A shows the relative lengths of the present ZmRb1 protein and the human retinoblastoma
35 proteins. The sub-figure B shows the alignment of the

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amino acids sequences of the Pocket A and Pocket B of the ZmRb1 with that of the Xenopus, chicken, rat and three human protein (Rb, p107 and p130).

Fig. 2. This figure is a map of the main characteristics of the WDV virus and the pWori vector derived from WDV and the positions of the deletions and mutations used in order to establish that the LXCXE motif is required for its replication in plants cells.

EXAMPLE 1.

Isolation of DNA and protein expressing clones.

Total RNA was isolated from maize root and mature leaves by grinding the material previously frozen in liquid nitrogen essentially as described in Soni et al (1995). The major and minor p75ZmRb1 mRNAs were identified by hybridization to a random-primed 32P-labelled PstI internal fragment (1.4 kb).

A portion of a maize cDNA library (106 pfu) in 12APII (Stratagene) was screened by subsequent hybridization to 5'-labelled oligonucleotides designed to be complementary to a known EST sequence of homologue maize of p130. These oligonucleotides were 5'-AATAGACACATCGATCAA/G (M.5m, nt positions 1411-1438) and 5'-GTAATGATACCAACATGG (M.3c, nt positions 1606-1590) (Isogen Biosciences).

After the second round of screening, pBluescript SK-(pBS) phagemids from positive clones were isolated by in vivo excision with ExAssist helper phage (Stratagene) according to protocols recommended by the manufacturer. DNA sequencing was carried out using a Sequenase™ Kit (USB).

The 5'-end of the mRNAs encoding p75ZmRb1 was determined by RACE-PCR. Poly-A+mRNA was purified by chromatography on oligo-dT-cellulose (Amersham). The first strand was synthesized using oligonucleotide DraI35 (5'-GATTTAAAATCAAGCTCC, nt positions 113-96). After denaturation at 90°C for 3 min, RNA was eliminated by

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RNase treatment, the cDNA recovered and 5'-tailed with terminal transferase and dATP. Then a PCR fragment was amplified using primer DraI35 and the linker-primer (50 bp) of the Stratagene cDNA synthesis kit.

5 One of the positive clones so produced contained a ~4 kb insert that, according to restriction analysis, extended both 5' and 3' of the region contained in the Expressed Sequence Tag used. The nucleotide sequence corresponding to the longest cDNA insert (3747 bp) is
10 shown in SEQ ID No. 1. This ZmRb1 cDNA contains a single open reading frame capable of encoding a protein of 683 amino acids (predicted Mr 75247, p75ZmRb1) followed by a 1646 bp 3'-untranslated region. Untranslated regions of similar length have been also found in mammalian Rb cDNAs
15 (Lee, W.-L. et al, Science 235, 1394 (1987); Bernards, R. et al, Proc. Natl. Acad. Sci. USA 86, 6474 (1989)). Northern analysis indicates that maize cells derived from both root meristems and mature leaves contain a major message, $\sim 2.7 \pm 0.2$ kb in length. In addition, a minor
20 $\sim 3.7 \pm 0.2$ kb message also appears. Heterogeneous transcripts have been detected in other species (Destrée, O. H. J. et al, Dev. Biol. 153, 141 (1992)).

Plasmid pWori $\Delta\Delta$ was constructed by deleting in pWori most of the sequences encoding WDV proteins (Sanz and
25 Gutierrez, unpublished). Plasmid p35S.Rb1 was constructed by inserting the CaMV 35S promoter (obtained from pWDV3:35SGUS) upstream of the ZmRb1 cDNA in the pBS vector. Plasmid p35S.130 was constructed by introducing the complete coding sequence of human p130 instead of
30 ZmRb1 sequences into p35S.Rb1. Plasmid p35.A+B was constructed by substituting sequences encoding the WDV RepA and RepB ORFs instead of ZmRb1 in p35S.Rb1 plasmid. (See Soni, R. and Murray, J. A. H. Anal. Biochem. 218, 474-476 (1994)).

35 The sequence around the methionine codon at nucleotide

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position 31 contains a consensus translation start (Kozak, M. J. Mol. Biol. 196, 947 (1987)). To determine whether the cDNA contained the full-length ZmRb1 coding region, the 5'-end of the mRNAs was amplified by RACE-PCR using an oligonucleotide derived from a region close to the putative initiator AUG, which would produce a fragment of ~150 bp. The results are consistent with the ZmRb1 cDNA clone containing the complete coding region.

The ZmRb1 protein contains segments homologous to the A and B subdomains of the "pocket" that is present in all members of the Rb family. These subdomains are separated by a non-conserved spacer. ZmRb1 also contains non-conserved N-terminal and C-terminal domains. Overall, ZmRb1 shares ~28-30% amino acid identity (~50% similarity) with the Rb family members (Hannon, G. J., Demetrick, D. & Beach, D. Genes Dev. 7, 2378 (1993); Cobrinik, D., Whyte, P., Peeper, D.S., Jacks, T. & Weinberg, R. A. *ibid.*, p. 2392 (1993). Ewen, M. E., Xing, Y. Lawrence, J. B. and Livingston, D. M. Cell 66, 1155 (1991))(Lee W. L. et al, Science 235, 1394 (1987); Bernards et al, Proc. Natl. Acad. Sci. USA 86, 6974 (1989)), with the A and B subdomains exhibiting the highest homology (~50-64%). Interestingly, amino acid C706 in human Rb, critical for its function (Kaye, F. J., Kratzke R. A., Gerster, J. L. and Horowitz, J. M. Proc. Natl. Acad. Sci. USA 87, 6922 (1990)), is also conserved in maize p75ZmRb1.

Note: The 561-577 amino acids encompass a proline-rich domain.

ZmRb1 contains 16 consensus sites, SP or TP for phosphorylation by cyclins dependant kinases (CDKs) with one of the 5'-tail of the sub-domain A and several in the C-terminal area which are potential sites of phosphorylation. A nucleic acid preferred group which encodes proteins in which one or more of these sites are

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changed or deleted, making the protein more resistant to the phosphorylation and thus, to its functionality, for example linking to E2F or similar. This can be easily carried out by means of mutagenesis conducted by means of PCR.

EXAMPLE 2

In vivo activity.

Replication of wheat dwarf geminivirus (WDV) is dependent upon an intact LXCXE motif of the viral RepA protein. This motif can mediate interaction with a member of the human Rb family, p130, in yeasts. Therefore, the inventors investigated whether p75ZmRb1 could complex with WDV RepA by using the yeast two-hybrid system (Fields, S. and Song, O. Nature 340, 245-246 (1989)). Yeast cells were co-transformed with a plasmid encoding the fusion GAL4BD-RepA protein and with plasmids encoding different GAL4AD fusion protein. The GAL4AD-p75ZmRb1 fusion could also complex with GAL4BD-RepA to allow growth of the recipient yeast cells in the absence of histidine. This interaction was slightly stronger than that seen with the human p130 protein. RepA could also bind to some extent to a N-terminally truncated form of p75ZmRb1. The role of the LXCXE motif in RepA-p75ZmRb1 interaction was assessed using a point mutation in WDV RepA (E198K) which we previously showed to destroy interaction with human p130. Co-transformation of ZmRb1 with a plasmid encoding the fusion GAL4BD-RepA(E198K) indicated that the interaction between RepA and p75ZmRb1 occurred through the LXCXE motif.

In this respect, the E198K mutant of WDV RepA behaves similarly to analogous point mutants of animal virus oncoproteins (Moran, E., Zerler, B., Harrison, T. M. and Mathews, M.B. Mol. Cell Biol. 6, 3470 (1986); Cherington, V. et al., *ibid.*, p. 1380 (1988); Lillie, J. W., Lowenstein, P. M., Green, M. R. and Green, M. Cell 50,

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1091 (1987); DeCarpio, J. A. et al., *ibid.*, p. 275 (1988)).

Specific interaction between maize p75ZmRb1 and WDV RepA in the yeast two-hybrid system (Fields et al) relied on the ability to reconstitute a functional GAL4 activity from two separated GAL4 fusion proteins containing the DNA binding domain (GAL4BD) and the activation domain (GAL4AD). Yeast HF7c cells were co-transformed with a plasmid expressing the GAL4BD-RepA or the GAL4BD-RepA(E198K) fusions and the plasmids expressing the GAL4AD alone (Vec) or fused to human p130, maize p75 (p75ZmRb1) or a 69 amino acids N-terminal deletion of p75 (p75ZmRb1-DN). Cells were streaked on plates with or without histidine according to the distribution shown in the upper left corner. The ability to grow in the absence of histidine depends on the functional reconstitution of a GAL4 activity upon interaction of the fusion proteins, since this triggers expression of the HIS3 gene which is under the control of a GAL4 responsive element. The growth characteristics of these yeast co-transformants correlate with the levels of b-galactosidase activity.

Procedures for two-hybrid analysis are described in Xie et al (1995). The GAL4AD-ZmRb1 fusions were construed in the pGAD424 vector.

EXAMPLE 3

In vivo activity.

Geminivirus DNA replication requires the cellular DNA replication machinery as well as other S-phase specific factors (Davies, J. W. and Stanley, J. *Trends Genet.* 5, 77 (1989); Lazarowitz, S. *Crit. Rev. Plant Sci.* 11, 327 (1992)). Consistent with this requirement, geminivirus infection appears to drive non-proliferating cells into S-phase, as indicated by the accumulation of the proliferating cell nuclear antigen (PCNA), a protein which is not normally present in the nuclei of

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differentiated cells (Nagar, S., Pedersen, T. J., Carrick, K. M., Hanley-Bowdoin, L. and Robertson, D. Plant Cell 7, 705 (1995)). The inventors finding that efficient WDV DNA replication requires an intact LXCXE motif in RepA coupled with the discovery of a plant homolog of Rb supports the model that, as in animal cells, sequestration of plant Rb by viral RepA protein promotes inappropriate entry of infected cells into S-phase. Therefore, one way to investigate the function of p75ZmRb1 was to measure geminivirus DNA replication in cells transfected with a plasmid bearing the ZmRb1 sequences under a promoter functional in plant cells, an approach analogous to that previously used in human cells (Uzvolgi, E. et al., Cell Growth Diff 2, 297 (1991)). Accumulation of newly replicated viral plasmid DNA was impaired in wheat cells transfected with plasmids expressing p75ZmRb1 or human p130, when expression of WDV replication protein(s) is directed wither by the WDV promoter or by the CaMV 35S promoter.

Since WDV DNA replication requires an S-phase cellular environment, interference with viral DNA replication by p75ZmRb1 and human p130 strongly evidences a role for retinoblastoma protein in the control of the G1/S transition in plants. The existence of a plant Rb homolog implies that despite their ancient divergence, plant and animal cells use, at least in part, similar regulatory proteins and pathways for cell cycle control.

Two lines of evidences reinforce this model. First, a gene encoding a protein that complements specifically the G1/S, but not the G2/M transition of the budding yeast cdc28 mutant has been identified in alfalfa cells (Hirt, H., Páy, A., Bögre, L., Meskiene, I. and Heberle-Bors, E. Plant J. 4, 61 (1993)). Second, plant homologs of D-type cyclins have been isolated from Arabidopsis and these, like their mammalian relatives, contain LXCXE motifs. In

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concert with plant versions of CDK4 and CDK6, plant D-type cyclins may regulate passage through G1 phase by controlling the phosphorylation state of Rb-like proteins.

5 In animal cells, the Rb family has been implicated in tumor suppression and in the control of differentiation and development. Thus, p75ZmRb1 could also play key regulatory roles at other levels during the plant cell life. One key question that is raised by the existence of
10 Rb homologs in plant cells is whether, as in animals disruption of the Rb pathway leads to a tumor-prone condition. In this regard, the inventors have noted that the VirB4 protein encoded by the Ti plasmids of both *Agrobacterium tumefaciens* and *A. rhizogenes* contains an
15 LXCXE motif. Although the VirB4 protein is required for tumor induction (Hooykas, P. J. J. and Beijersbergen, A. G. M. Annu. Rev. Phytopathol. 32, 157 (1994), the function of its LXCXE motif in this context remains to be examined. Geminivirus infection is not accompanied by
20 tumor development in the infected plant, but in some cases an abnormal growth of enations has been observed (G. Dafalla and B. Gronenborn, personal communication).

Inhibition of wheat dwarf geminivirus (WDV) DNA replication by ZmRb1 or human p130 in cultured wheat
25 cells was carried out as follows. A. Wheat cells were transfected, as indicated, with pWori (Xie et al. 1995) alone (0.5g), a replicating WDV-based plasmid which encodes WDV proteins required for viral DNA replication, and with control plasmid pBS (10 g) or p35S.Rb1 (10 g),
30 which encodes ZmRb1 sequences under the control of the CaMV 35S promoter. Total DNA was purified one and two days after transfection, equal amounts fractionated in agarose gels and ethidium bromide staining and viral pWori DNA identified by Southern hybridization. Plasmid
35 DNA represents exclusively newly-replicated plasmid DNA

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since it is fully resistant to DpnI digestion and sensitive to MboI. Note that the MboI-digested samples were run for about half of the length than the undigested samples. B. To test the effect of human p130 on WDV DNA replication, wheat cells were co-transfected with pWori (0.5 g) and plasmids pBS (control), p35S.Rb1 or p35S.130 (10 g in each case). Replication of the test plasmid (pWori) was analyzed two days after transfection and was detected as described in part A using ethidium bromide staining; and Southern hybridization. C. To test the effect of ZmRb1 or human p130 on WDV DNA replication when expression of viral proteins was directed by the CaMV 35S promoter, the test plasmid pWori $\Delta\Delta$ (which does not encode functional WDV replication proteins but replicates when they are provided by a different plasmid, i. e. pWori) was used. Wheat cells were co-transfected, as indicated, with pWori $\Delta\Delta$ (0.25 g), pWori (0.25 g), p35S.A+B (6 g), p35S.Rb1 (10 g) and/or p35S.130 (10 g). Replication of the test plasmid (pWori $\Delta\Delta$) was analyzed 36 hours after transfection and was detected as described in part A using ethidium bromide staining; Southern hybridization. Plasmids pWori (M1) and pWori $\Delta\Delta$ (M2; Sanz and Gutiérrez, unpublished), 100 pg in each case, were used as markers. Suspension cultures of wheat cells, transfection by particle bombardment and analysis of viral DNA replication were carried out as described in (Xie et al. 1995), except that DNA extraction was modified as in (Soni and Murray. *Anal. Biochem.* 218, 474-476 (1995)).

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

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5 (A) NAME: QI XIE

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(C) CITY: MADRID

10 (E) COUNTRY: SPAIN

(F) POSTAL CODE (ZIP): 28049

(ii) TITLE OF THE INVENTION: PLANT PROTEINS

(iii) NUMBER OF SEQUENCES: 2

15 (iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

20 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3747 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

30 (iv) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Zea mays

(ix) FEATURE:

35 (A) NAME/KEY: CDS

- 15 -

(B) LOCATION: 31..2079

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GAATTCGGCA CGAGCAAAGG TCTGATTGAT ATG GAA TGT TTC CAG TCA AAT TTG	54
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1 5	
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Glu Lys Met Glu Lys Leu Cys Asn Ser Asn Ser Cys Lys Gly Glu Leu	
10 15 20	
GAT TTT AAA TCA ATT TTG ATC AAT AAT GAT TAT ATT CCC TAT GAT GAG	150
Asp Phe Lys Ser Ile Leu Ile Asn Asn Asp Tyr Ile Pro Tyr Asp Glu	
25 30 35 40	
AAC TCG ACG GGG GAT TCC ACC AAT TTA GGA CAT TCA AAG TGT GCC TTT	198
Asn Ser Thr Gly Asp Ser Thr Asn Leu Gly His Ser Lys Cys Ala Phe	
45 50 55	
GAA ACA TTG GCA TCT CCC ACA AAG ACA ATA AAG AAC ATG CTG ACT GTT	246
Glu Thr Leu Ala Ser Pro Thr Lys Thr Ile Lys Asn Met Leu Thr Val	
60 65 70	
CCT AGT TCT CCT TTG TCA CCA GCC ACC GGT GGT TCA GTC AAG ATT GTG	294
Pro Ser Ser Pro Leu Ser Pro Ala Thr Gly Gly Ser Val Lys Ile Val	
75 80 85	
CAA ATG ACA CCA GTA ACT TCT GCC ATG ACG ACA GCT AAG TGG CTT CGT	342
Gln Met Thr Pro Val Thr Ser Ala Met Thr Thr Ala Lys Trp Leu Arg	
90 95 100	
GAG GTG ATA TCT TCA TTG CCA GAT AAG CCT TCA TCT AAG CTT CAG CAG	390
Glu Val Ile Ser Ser Leu Pro Asp Lys Pro Ser Ser Lys Leu Gln Gln	
105 110 115 120	
TTT CTG TCA TCA TGC GAT AGG GAT TTG ACA AAT GCT GTC ACA GAA AGG	438
Phe Leu Ser Ser Cys Asp Arg Asp Leu Thr Asn Ala Val Thr Glu Arg	
125 130 135	
GTC AGC ATA GTT TTG GAA GCA ATT TTT CCA ACC AAA TCT TCT GCC AAT	486
Val Ser Ile Val Leu Glu Ala Ile Phe Pro Thr Lys Ser Ser Ala Asn	
140 145 150	
CGG GGT GTA TCG TTA GGT CTC AAT TGT GCA AAT GCC TTT GAC ATT CCG	534
Arg Gly Val Ser Leu Gly Leu Asn Cys Ala Asn Ala Phe Asp Ile Pro	
155 160 165	
TGG GCA GAA GCC AGA AAA GTG GAG GCT TCC AAG TTG TAC TAT AGG GTA	582
Trp Ala Glu Ala Arg Lys Val Glu Ala Ser Lys Leu Tyr Tyr Arg Val	
170 175 180	

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TTA	GAG	GCA	ATC	TGC	AGA	GCG	GAG	TTA	CAA	AAC	AGC	AAT	GTA	AAT	AAT	630
Leu	Glu	Ala	Ile	Cys	Arg	Ala	Glu	Leu	Gln	Asn	Ser	Asn	Val	Asn	Asn	
185					190					195					200	
CTA	ACT	CCA	TTG	CTG	TCA	AAT	GAG	CGT	TTC	CAC	CGA	TGT	TTG	ATT	GCA	678
Leu	Thr	Pro	Leu	Leu	Ser	Asn	Glu	Arg	Phe	His	Arg	Cys	Leu	Ile	Ala	
				205					210						215	
TGT	TCA	GCG	GAC	TTA	GTA	TTG	GCG	ACA	CAT	AAG	ACA	GTC	ATC	ATG	ATG	726
Cys	Ser	Ala	Asp	Leu	Val	Leu	Ala	Thr	His	Lys	Thr	Val	Ile	Met	Met	
			220					225					230			
TTT	CCT	GCT	GTT	CTT	GAG	AGT	ACC	GGT	CTA	ACT	GCA	TTT	GAT	TTG	AGC	774
Phe	Pro	Ala	Val	Leu	Glu	Ser	Thr	Gly	Leu	Thr	Ala	Phe	Asp	Leu	Ser	
			235				240						245			
AAA	ATA	ATT	GAG	AAC	TTT	GTG	AGA	CAT	GAA	GAG	ACC	CTC	CCA	AGA	GAA	822
Iys	Ile	Ile	Glu	Asn	Phe	Val	Arg	His	Glu	Glu	Thr	Leu	Pro	Arg	Glu	
			250				255						260			
TTG	AAA	AGG	CAC	CTA	AAT	TCC	TTA	GAA	GAA	CAG	CTT	TTG	GAA	AGC	ATG	870
Leu	Iys	Arg	His	Leu	Asn	Ser	Leu	Glu	Glu	Gln	Leu	Leu	Glu	Ser	Met	
265					270					275					280	
GCA	TGG	GAG	AAA	GGT	TCA	TCA	TTG	TAT	AAC	TCA	CTG	ATT	GTT	GCC	AGG	918
Ala	Trp	Glu	Lys	Gly	Ser	Ser	Leu	Tyr	Asn	Ser	Leu	Ile	Val	Ala	Arg	
				285					290						295	
CCA	TCT	GTT	GCT	TCA	GAA	ATA	AAC	CGC	CTT	GGT	CTT	TTG	GCT	GAA	CCA	966
Pro	Ser	Val	Ala	Ser	Glu	Ile	Asn	Arg	Leu	Gly	Leu	Leu	Ala	Glu	Pro	
			300					305					310			
ATG	CCA	TCT	CTT	GAT	GAC	TTA	GTG	TCA	AGG	CAG	AAT	GTT	CGT	ATC	GAG	1014
Met	Pro	Ser	Leu	Asp	Asp	Leu	Val	Ser	Arg	Gln	Asn	Val	Arg	Ile	Glu	
			315				320						325			
GGC	TTG	CCT	GCT	ACA	CCA	TCT	AAA	AAA	CGT	GCT	GCT	GGT	CCA	GAT	GAC	1062
Gly	Leu	Pro	Ala	Thr	Pro	Ser	Lys	Lys	Arg	Ala	Ala	Gly	Pro	Asp	Asp	
			330				335					340				
AAC	GCT	GAT	CCT	CGA	TCA	CCA	AAG	AGA	TCG	TGC	AAT	GAA	TCT	AGG	AAC	1110
Asn	Ala	Asp	Pro	Arg	Ser	Pro	Lys	Arg	Ser	Cys	Asn	Glu	Ser	Arg	Asn	
345					350					355					360	
ACA	GTA	GTA	GAG	CGC	AAT	TTG	CAG	ACA	CCT	CCA	CCC	AAG	CAA	AGC	CAC	1158
Thr	Val	Val	Glu	Arg	Asn	Leu	Gln	Thr	Pro	Pro	Pro	Lys	Gln	Ser	His	
				365					370					375		
ATG	GTG	TCA	ACT	AGT	TTG	AAA	GCA	AAA	TGC	CAT	CCA	CTC	CAG	TCC	ACA	1206
Met	Val	Ser	Thr	Ser	Leu	Lys	Ala	Lys	Cys	His	Pro	Leu	Gln	Ser	Thr	
			380					385					390			
TTT	GCA															

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Phe	Ala	Ser	Pro	Thr	Val	Cys	Asn	Pro	Val	Gly	Gly	Asn	Glu	Lys	Cys	
	395						400						405			
GCT	GAC	GTG	ACA	ATT	CAT	ATA	TTC	TTT	TCC	AAG	ATT	CTG	AAG	TTG	GCT	1302
Ala	Asp	Val	Thr	Ile	His	Ile	Phe	Phe	Ser	Lys	Ile	Leu	Lys	Leu	Ala	
	410					415					420					
GCT	ATT	AGA	ATA	AGA	AAC	TTG	TGC	GAA	AGG	GTT	CAA	TGT	GTG	GAA	CAG	1350
Ala	Ile	Arg	Ile	Arg	Asn	Leu	Cys	Glu	Arg	Val	Gln	Cys	Val	Glu	Gln	
	425				430					435				440		
ACA	GAG	CGT	GTC	TAT	AAT	GTC	TTC	AAG	CAG	ATT	CTT	GAG	CAA	CAG	ACA	1398
Thr	Glu	Arg	Val	Tyr	Asn	Val	Phe	Lys	Gln	Ile	Leu	Glu	Gln	Gln	Thr	
			445					450						455		
ACA	TTA	TTT	TTT	AAT	AGA	CAC	ATC	GAT	CAA	CTT	ATC	CTT	TGC	TGT	CTT	1446
Thr	Leu	Phe	Phe	Asn	Arg	His	Ile	Asp	Gln	Leu	Ile	Leu	Cys	Cys	Leu	
		460					465						470			
TAT	GGT	GTT	GCA	AAG	GTT	TGT	CAA	TTA	GAA	CTC	ACA	TTT	AGG	GAG	ATA	1494
Tyr	Gly	Val	Ala	Lys	Val	Cys	Gln	Leu	Glu	Leu	Thr	Phe	Arg	Glu	Ile	
	475					480						485				
CTC	AAC	AAT	TAC	AAA	AGA	GAA	GCA	CAA	TGC	AAG	CCA	GAA	GTT	TTT	TCA	1542
Leu	Asn	Asn	Tyr	Lys	Arg	Glu	Ala	Gln	Cys	Lys	Pro	Glu	Val	Phe	Ser	
	490					495					500					
AGT	ATC	TAT	ATT	GGG	AGT	ACG	AAC	CGT	AAT	GGG	GTA	TTA	GTA	TCG	CGC	1590
Ser	Ile	Tyr	Ile	Gly	Ser	Thr	Asn	Arg	Asn	Gly	Val	Leu	Val	Ser	Arg	
	505				510					515				520		
CAT	GTT	GGT	ATC	ATT	ACT	TTT	TAC	AAT	GAG	GTA	TTT	GTT	CCA	GCA	GCG	1638
His	Val	Gly	Ile	Ile	Thr	Phe	Tyr	Asn	Glu	Val	Phe	Val	Pro	Ala	Ala	
			525					530				535				
AAG	CCT	TTC	CTG	GTG	TCA	CTA	ATA	TCA	TCT	GGT	ACT	CAT	CCA	GAA	GAC	1686
Lys	Pro	Phe	Leu	Val	Ser	Leu	Ile	Ser	Ser	Gly	Thr	His	Pro	Glu	Asp	
		540						545				550				
AAG	AAG	AAT	GCT	AGT	GGC	CAA	ATT	CCT	GGA	TCA	CCC	AAG	CCA	TCT	CCT	1734
Lys	Lys	Asn	Ala	Ser	Gly	Gln	Ile	Pro	Gly	Ser	Pro	Lys	Pro	Ser	Pro	
	555					560						565				
TTT	CCA	AAT	TTA	CCA	GAT	ATG	TCC	CCG	AAG	AAA	GTT	TCA	GCA	TCT	CAT	1782
Phe	Pro	Asn	Leu	Pro	Asp	Met	Ser	Pro	Lys	Lys	Val	Ser	Ala	Ser	His	
	570					575					580					
AAT	GTA	TAT	GTG	TCT	CCT	TTG	CGG	CAA	ACC	AAG	TTG	GAT	CTA	CTG	CTG	1830
Asn	Val	Tyr	Val	Ser	Pro	Leu	Arg	Gln	Thr	Lys	Leu	Asp	Leu	Leu	Leu	
	585				590					595				600		

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TCA CCA AGT TCC AGG AGT TTT TAT GCA TGC ATT GGT GAA GGC ACC CAT Ser Pro Ser Ser Arg Ser Phe Tyr Ala Cys Ile Gly Glu Gly Thr His 605 610 615	1878
GCT TAT CAG AGC CCA TCT AAG GAT TTG GCT GCT ATA AAT AGC CGC CTA Ala Tyr Gln Ser Pro Ser Lys Asp Leu Ala Ala Ile Asn Ser Arg Leu 620 625 630	1926
AAT TAT AAT GGC AGG AAA GTA AAC AGT CGA TTA AAT TTC GAC ATG GTG Asn Tyr Asn Gly Arg Lys Val Asn Ser Arg Leu Asn Phe Asp Met Val 635 640 645	1974
AGT GAC TCA GTG GTA GCC GGC AGT CTG GGC CAG ATA AAT GGT GGT TCT Ser Asp Ser Val Val Ala Gly Ser Leu Gly Gln Ile Asn Gly Gly Ser 650 655 660	2022
ACC TCG GAT CCT GCA GCT GCA TTT AGC CCC CTT TCA AAG AAG AGA GAG Thr Ser Asp Pro Ala Ala Ala Phe Ser Pro Leu Ser Lys Lys Arg Glu 665 670 675 680	2070
ACA GAT ACT TGATCAATTA TAAATGGTGG CCTCTCTCGT ATATAGCTCA Thr Asp Thr	2119
CAGATCCGTG CTCCTAGCA GTCTATTCTT CTGAATAAGT GGATTAACTG GAGCGATTTA	2179
ACTGTACATG TATGTGTTAG TGAGAAGCAG CAGTTTTTAG GCAGCAAAC GTTCAAGTT	2239
AGTTTTGAG CTATACCAT TTCTCTGCTG ATTGAACATA TCCGCTGTGT AGAGTGCTAA	2299
TGAATCTTA GTTTTCATTG GGCTGACATA ACAAATCTTT ATCCTAGTTG GCTGGTTGTT	2359
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TGATCCATA TTCAGTGTGC TGCAAGTGAT TTGACCATAT GTGGCTTATC CTTCAGGTAT	2659
GTCTCATGTT GTGACTTCAT TGCTGATTGC TTTTGTAATG GTACTGTTGA GTTCATTTCT	2719
GGTTACAATC AGCCTTTACT GCTTTATATT GTTCTACTAA TTTGGCTTG CACAGCCAGG	2779
ACGATTGGTT TTCTGCATCA ATCAATCTTT TTTAGGACAA GATATTTTGG TATGCTACAC	2839
TTCCCAAATT GCAATTATC CAGAAGCTA CCTTGTTTTA TTCTATTAGT TCTCAGCAAC	2899
AGTGAATGAA TATGAATCAG TCATGCTGAT AGATGTTTAT CTGGTTATTC CAAACAATCT	2959
GACATCGCAT CTCTTTCTGC AAGTGAGATG AAGAAAACCT GAAATGCTAT CACCATTTAA	3019

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AACATTGCCT TCTGGAAGTT CAGGTGATTA GCAGGAGACG TTCTGACATT GCCATTGACA 3079
TGTACGGTAG TGATGGCAGG AGACGTTCTT AAACAGCAGC TGCTCCTTCA GCTTGTAATG 3139
TCTGATTGTA TTGACCAAGA GCATCCACCT TGCCTTATGG TACTAACTGA ATGAGCTGGT 3199
GACGCTGACT CATCTGCATA ATGGCAGATG CTTAACCATC TTTAGGAGCT CATGTCATGA 3259
TTCCAGCTGC ACCGTGTCAA ATGTGAAGGC CCTGCAAGGC TTTCCAGGCC GCACCAATCC 3319
TGCTTGCTTC TTGAAGATAC ATATGGTGCC ACCTAAATAA AAGCTGTTTC TGGTTATGTC 3379
TGTCCTTGAC ATGTCAACAG ATTAGTGTG GGTGTCAGTC ATGTGGTGTT TAACTCTTGG 3439
AGAAGGCGAG AAGTCATTGC TGCCAGCATT GTGATCGTCA GGCACAGAAG TACTCAAAAG 3499
TGAGAGCTAC TTGTTGCGAG CAAACGGAGG GCGATATAGG TTGATAGCCA ATTCAGTTC 3559
TCTATATACA AGCAGCGGAT TTTGTTTAGA GTTAGCTTTT GAGATGCATC ATTTCTTTCA 3619
CATCTGATTC TGTGTGTTGT AACTCGGAGT CGCGTAGAAG TTAGAATGCT AACTGACCTT 3679
AATTTTCACC GAATAATTG CTAGCGTTTT TCAGTATGAA ATCCTTGTC TAAAAAAA 3739
AAAAAAA 3747

```

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 683 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

```

Met Glu Cys Phe Gln Ser Asn Leu Glu Lys Met Glu Lys Leu Cys Asn
 1             5             10             15

Ser Asn Ser Cys Lys Gly Glu Leu Asp Phe Lys Ser Ile Leu Ile Asn
20             25             30

Asn Asp Tyr Ile Pro Tyr Asp Glu Asn Ser Thr Gly Asp Ser Thr Asn
35             40             45

Leu Gly His Ser Lys Cys Ala Phe Glu Thr Leu Ala Ser Pro Thr Lys
50             55             60

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Thr Ile Lys Asn Met Leu Thr Val Pro Ser Ser Pro Leu Ser Pro Ala
 65 70 75 80

Thr Gly Gly Ser Val Lys Ile Val Gln Met Thr Pro Val Thr Ser Ala
 85 90 95

Met Thr Thr Ala Lys Trp Leu Arg Glu Val Ile Ser Ser Leu Pro Asp
 100 105 110

Lys Pro Ser Ser Lys Leu Gln Gln Phe Leu Ser Ser Cys Asp Arg Asp
 115 120 125

Leu Thr Asn Ala Val Thr Glu Arg Val Ser Ile Val Leu Glu Ala Ile
 130 135 140

Phe Pro Thr Lys Ser Ser Ala Asn Arg Gly Val Ser Leu Gly Leu Asn
 145 150 155 160

Cys Ala Asn Ala Phe Asp Ile Pro Trp Ala Glu Ala Arg Lys Val Glu
 165 170 175

Ala Ser Lys Leu Tyr Tyr Arg Val Leu Glu Ala Ile Cys Arg Ala Glu
 180 185 190

Leu Gln Asn Ser Asn Val Asn Asn Leu Thr Pro Leu Leu Ser Asn Glu
 195 200 205

Arg Phe His Arg Cys Leu Ile Ala Cys Ser Ala Asp Leu Val Leu Ala
 210 215 220

Thr His Lys Thr Val Ile Met Met Phe Pro Ala Val Leu Glu Ser Thr
 225 230 235 240

Gly Leu Thr Ala Phe Asp Leu Ser Lys Ile Ile Glu Asn Phe Val Arg
 245 250 255

His Glu Glu Thr Leu Pro Arg Glu Leu Lys Arg His Leu Asn Ser Leu
 260 265 270

Glu Glu Gln Leu Leu Glu Ser Met Ala Trp Glu Lys Gly Ser Ser Leu
 275 280 285

Tyr Asn Ser Leu Ile Val Ala Arg Pro Ser Val Ala Ser Glu Ile Asn
 290 295 300

Arg Leu Gly Leu Leu Ala Glu Pro Met Pro Ser Leu Asp Asp Leu Val
 305 310 315 320

Ser Arg Gln Asn Val Arg Ile Glu Gly Leu Pro Ala Thr Pro Ser Lys
 325 330 335

Lys Arg Ala Ala Gly Pro Asp Asp Asn Ala Asp Pro Arg Ser Pro Lys
 340 345 350

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Arg Ser Cys Asn Glu Ser Arg Asn Thr Val Val Glu Arg Asn Leu Gln
 355 360 365
 Thr Pro Pro Pro Lys Gln Ser His Met Val Ser Thr Ser Leu Lys Ala
 370 375 380
 Lys Cys His Pro Leu Gln Ser Thr Phe Ala Ser Pro Thr Val Cys Asn
 385 390 395 400
 Pro Val Gly Gly Asn Glu Lys Cys Ala Asp Val Thr Ile His Ile Phe
 405 410 415
 Phe Ser Lys Ile Leu Lys Leu Ala Ala Ile Arg Ile Arg Asn Leu Cys
 420 425 430
 Glu Arg Val Gln Cys Val Glu Gln Thr Glu Arg Val Tyr Asn Val Phe
 435 440 445
 Lys Gln Ile Leu Glu Gln Gln Thr Thr Leu Phe Phe Asn Arg His Ile
 450 455 460
 Asp Gln Leu Ile Leu Cys Cys Leu Tyr Gly Val Ala Lys Val Cys Gln
 465 470 475 480
 Leu Glu Leu Thr Phe Arg Glu Ile Leu Asn Asn Tyr Lys Arg Glu Ala
 485 490 495
 Gln Cys Lys Pro Glu Val Phe Ser Ser Ile Tyr Ile Gly Ser Thr Asn
 500 505 510
 Arg Asn Gly Val Leu Val Ser Arg His Val Gly Ile Ile Thr Phe Tyr
 515 520 525
 Asn Glu Val Phe Val Pro Ala Ala Lys Pro Phe Leu Val Ser Leu Ile
 530 535 540
 Ser Ser Gly Thr His Pro Glu Asp Lys Lys Asn Ala Ser Gly Gln Ile
 545 550 555 560
 Pro Gly Ser Pro Lys Pro Ser Pro Phe Pro Asn Leu Pro Asp Met Ser
 565 570 575
 Pro Lys Lys Val Ser Ala Ser His Asn Val Tyr Val Ser Pro Leu Arg
 580 585 590
 Gln Thr Lys Leu Asp Leu Leu Leu Ser Pro Ser Ser Arg Ser Phe Tyr
 595 600 605
 Ala Cys Ile Gly Glu Gly Thr His Ala Tyr Gln Ser Pro Ser Lys Asp
 610 615 620
 Leu Ala Ala Ile Asn Ser Arg Leu Asn Tyr Asn Gly Arg Lys Val Asn
 625 630 635 640

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Ser Arg Leu Asn Phe Asp Met Val Ser Asp Ser Val Val Ala Gly Ser
645 650 655

Leu Gly Gln Ile Asn Gly Gly Ser Thr Ser Asp Pro Ala Ala Ala Phe
660 665 670

Ser Pro Leu Ser Lys Lys Arg Glu Thr Asp Thr
675 680

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INFORMATION RELATIVE TO THE DEPOSIT OF A MICRO-ORGANISM

The micro-organism to which reference is made in page 6 of the disclosure has been deposited in the following institution:

5 COLECCION ESPAÑOLA DE CULTIVOS TIPO (CECT)

Departamento de Microbiología
Facultad de Ciencias Biológicas
46100 BURJASOT (Valencia)
Spain

10 Deposit identification: pBS.Rb1

Deposit date: June 12, 1996

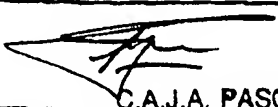
Order No.: 4699

This information appears reflected in the form PCE/RO/134 enclosed to the request.

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INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page <u>6</u> , line <u>24</u> and following	
B. IDENTIFICATION OF DEPOSIT <u>pBS.Rb1</u> Further deposits are identified on an additional sheet <input type="checkbox"/>	
Name of depositary institution <u>COLECCION ESPAÑOLA DE CULTIVOS TIPO (CECT)</u>	
Address of depositary institution (including postal code and country) <u>Departamento de Microbiología</u> <u>Facultad de Ciencias Biológicas</u> <u>46100 BURJASOT (Valencia)</u> <u>Spain</u>	
Date of deposit <u>12 June 1996</u>	Accession Number <u>4699</u>
C. ADDITIONAL INDICATIONS (leave blank if not applicable) This information is continued on an additional sheet <input type="checkbox"/>	
D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)	
E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)	
The indications listed below will be submitted to the International Bureau later (specify the general nature of the indications e.g. "Accession Number of Deposit")	
For receiving Office use only <input checked="" type="checkbox"/> This sheet was received with the international application Authorized officer  <u>C.A.J.A. PASCHE</u>	For International Bureau use only <input type="checkbox"/> This sheet was received by the International Bureau on: Authorized officer

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CLAIMS

1. Use of a retinoblastoma (Rb) protein for the control
of the growth and/or replication of plant cells and plant
5 viruses.

2. Use as claimed in claim 1 characterised in that the
virus requires the integrity of an LXCXE amino acid motif
in one of its proteins for the normal reproduction.

10 3. Use as claimed in claim 1 wherein the virus is a
Geminivirus.

4. Use in accordance with claim 1 characterised in that
15 the virus binds a retinoblastoma (Rb) protein in order to
release a transcription factor.

5. A method of controlling the growth and/or replication
of a plant cell or a plant virus within that cell,
20 comprising the increase or decrease of the level and/or
activity of a retinoblastoma protein in that plant cell.

6. A method as claimed in claim 5 characterised in that
the level of protein is increased by direct application.

25 7. A method as claimed in claim 5 characterised in that
the level of protein is increased by introduction of DNA
or RNA encoding for its expression into the plant cell
which it is desired to treat.

30 8. A method as claimed in claim 5, 6 or 7 wherein the
protein is overexpressed.

9. A method of controlling the growth and/or replication
35 of a plant cell or a plant virus comprising expressing an

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Rb protein, or peptide fragment thereof that interacts with the LXCXE motif of the virus but does not affect the normal functioning of the cell, such as to inhibit cell growth or normal viral growth.

5

10. Recombinant nucleic acid encoding for expression of an Rb protein that has one or more characteristics of plant Rb protein not shared by animal Rb protein.

10

11. Nucleic acid as claimed in claim 10 characterised in that it comprises one or more characteristic regions that differ from known animal Rb protein nucleic acid.

15

12. Recombinant nucleic acid in the form of DNA or cRNA which encodes for a plant Rb protein having A and B pocket subdomains having a sequence with between 30% and 75% homology with human Rb protein.

20

13. Nucleic acid as claimed in claim 12 having a sequence with between 30% and 75% homology with p130 Rb retinoblastoma protein.

25

14. Nucleic acid as claimed in claim 12 or 13 characterised in that it has from 50% to 64% homology with animal or p130 Rb retinoblastoma protein.

15. Nucleic acid as claimed in any one of claims 12 to 14 encoding for the C706 amino acid of human Rb.

30

16. Nucleic acid as claimed in any one of claims 12 to 15 wherein the spacer sequence between the A and B pockets is not conserved with respect to animal Rb proteins.

35

17. Nucleic acid as claimed in claim 16 wherein the spacer sequence has less than 50% homology to the same

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region found in animal retinoblastoma proteins.

18. Nucleic acid as claimed in any one of claims 12 to 17 having 80% or more homology with that of SEQ NO 2.

5

19. Nucleic acid as claimed in claim 18 wherein the homology is 90% or more.

10

20. Recombinant DNA comprising a sequence corresponding to SEQ ID No 1 bases 31 to 2079.

21. Recombinant DNA comprising a sequence corresponding to SEQ ID No 1 or corresponding RNA encoding for maize cDNA clone encoding ZmRb1 of SQ ID No 2.

15

22. Protein encoded by the recombinant DNA or RNA as claimed in any one of claims 12 to 21 or novel proteins derived from such DNA or RNA, and protein derived from naturally occurring DNA or RNA altered by mutagenic means.

20

23. Protein as claimed in claim 22 wherein the mutagenic means comprises mutagenesis using mutagenic PCR primers.

25

24. Anti-sense DNA or RNA of a gene encoding for a plant retinoblastoma protein, a gene which possesses the nucleic acid sequence as the one which is claimed in any one of the claims 10 to 21.

30

25. Vectors, cells, plants or animals comprising the DNA or RNA as claimed in any one of claims 12 to 22.

35

26. A method to control the growth and/or the proliferation of a vegetable cell or of a plant virus comprising the decrease of plant retinoblastoma protein

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levels in the cell by incorporation to this cell of anti-sense DNA or RNA to the retinoblastoma protein.

5 27. cDNA encoding a protein as it is claimed in the claim 22.

10 28. A nucleic acid encoding a protein in which one or more of these sites are altered or deleted, making the protein more resistant to the phosphorylation and thus, to its functionality, for example, linking to E2F or similar.

15 29. An encoded protein by the nucleic acid which is described in claim 28.

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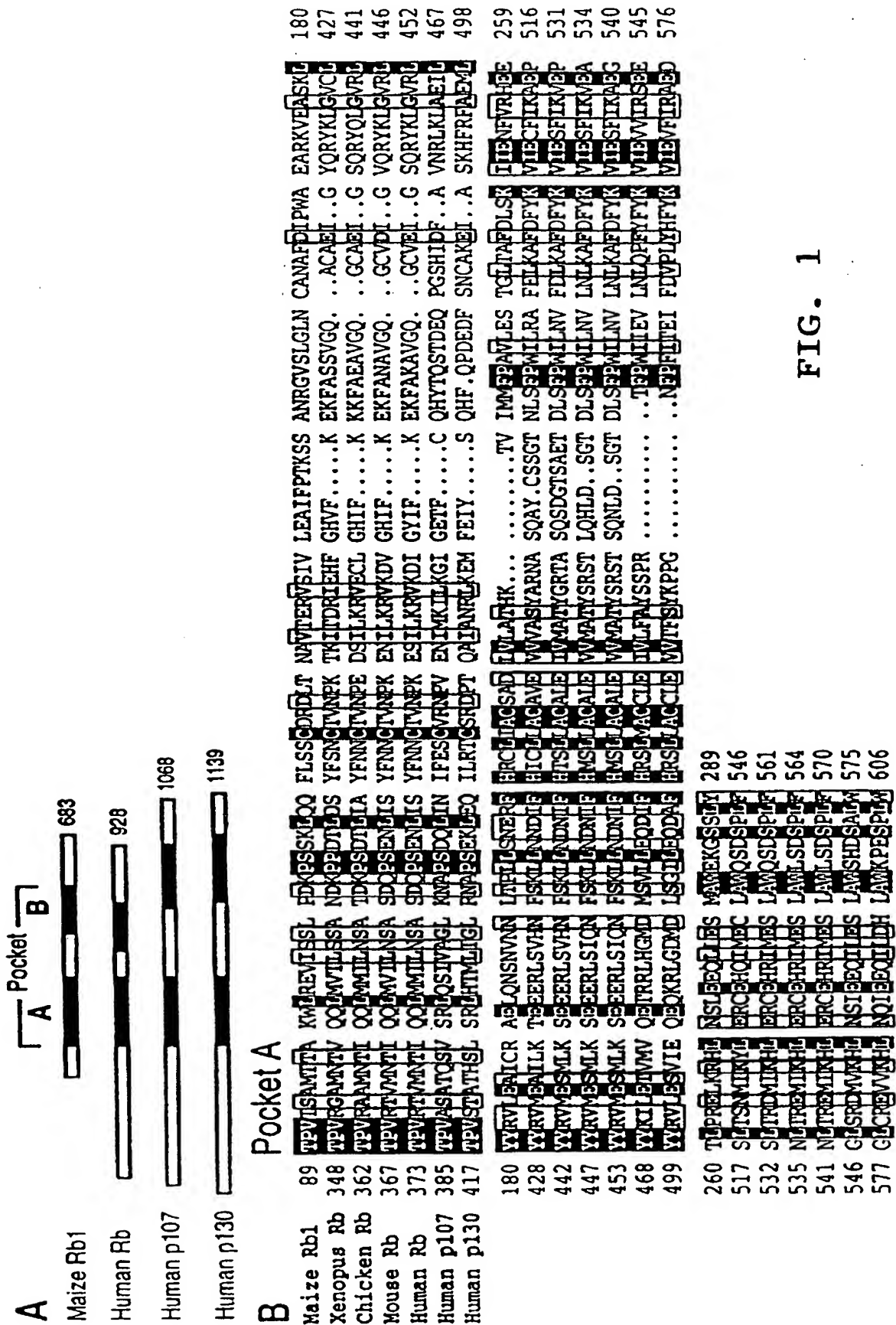


FIG. 1

BEST AVAILABLE

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Pocket B

Maize Rb1	405	NEKCAVTH	IFESKILKA	AIRIRNICER	VCQ..VEDTE	RVYVNFQKID	EQQTIFPFR	HIDQILICCL	VGVARVCOLE	LTEREHLNNV	492
Xenopus Rb	614	QKSTSL..	IFYKKVYLA	YKRISLSCSS	LLSDHPELEQ	VINTLLOHTL	QOEYELMRDR	HIDQIMCSM	YGICRAKNID	LREKTIIVTAV	701
Chicken Rb	630	QKPKSTSL	IFYKKVYLA	YLRITLFFR	LLSEHPDLEP	LINTLFOHTL	QNESELMRDR	HIDQIMCSM	YGICKVKNVD	LREKTIIVTAV	719
Mouse Rb	632	QKPLKSTSLA	IFYKKVYLA	YLRITLFCAR	LLSDHPELEH	IINTLFOHTL	QNEYELMRDR	HIDQIMCSM	YGICKVKNID	LKEKIIIVTAV	721
Human Rb	639	QKPLKSTSL	IFYKKVYLA	YLRITLFCER	LLSEHPLEH	IINTLFOHTL	QNEYELMRDR	HIDQIMCSM	YGICKVKNID	LKEKIIIVTAV	728
Human p107	780	NRPKRTGSLA	IFYKKVYLA	SVRLDCLCK	LDVSN..ELRR	KIMTCFEFTL	VHCPDLMRDR	HIDQILICAF	YIMAKVTKEE	RTQOEIMKSV	868
Human p130	828	NRPKRTSLS	IFYKKVYLA	AVRLDCLCAK	LDISD..ELRK	KIMTCFEFTL	IQCPDLMRDR	HIDQILICAI	YIMAKVTKEE	KSEONIMRCY	916
	493	PREAQCKPEV	FSSIMF...GSTNRNG	VLVSRHVGIN	525
	702	KGLTNTNQET	FKHWLIR...DQHQDSII	726
	720	KELPNTNQET	FKRWLIR...EEQYDSII	744
	722	KDLPHAAQET	FKRWLIR...EEEFDSII	746
	729	KDLPHAVQET	FKRWLIK...EEYDSDII	753
	869	RNQPQANSHV	YFSWLK...	...	SIP REVVAYNKNI	NDDFEMID..CDEED	ATKTPDCSSG	PVKEERSDLI	931
	917	ETQPQARSQV	YFSWLKKGKR	KRRNSGSDS	RSQNSPTL	NKDRTSRDSS	PVMRSSTLP	VPOPSSAPPT	PTRLTGANSND	MEEEERGDLI	1006
	526	TEVNEVTPA	APFFLV	541							
	727	VEVNLVFMQK	LKSHIL	742							
	745	VEVNLVFMQK	LKTNIL	760							
	747	VEVNLVFMQK	LKTNIL	762							
	754	VEVNLVFMQK	LKTNIL	769							
	932	KEVNTIYNGR	VNSFAL	947							
	1007	QETNNTIYKQ	IKTFAM	1002							

FIG. 1

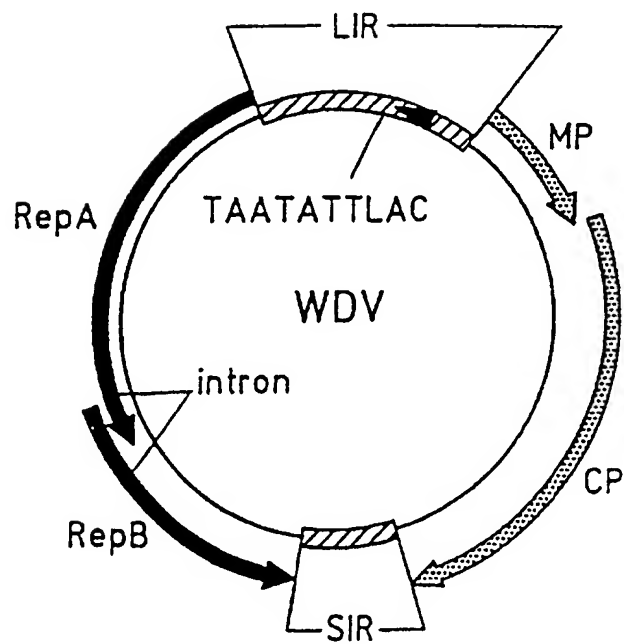
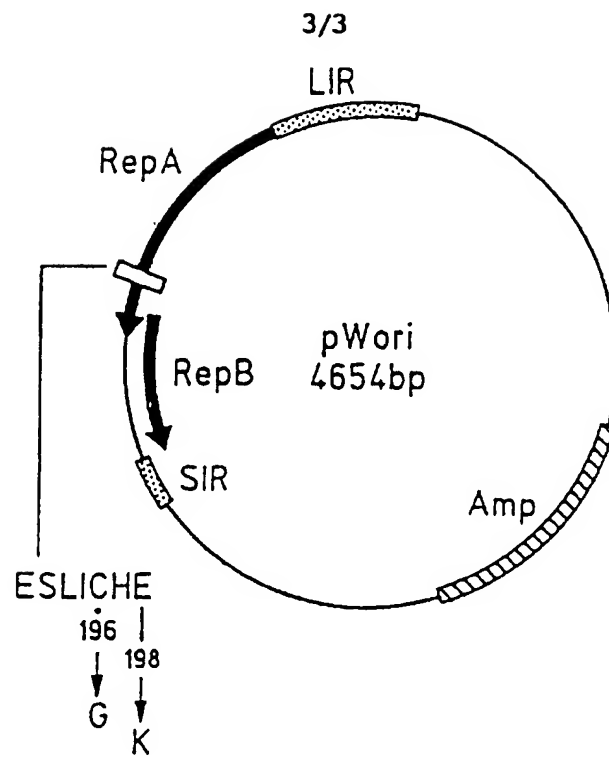


Fig. 2

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 97/03070

A. CLASSIFICATION OF SUBJECT MATTER

IPC 6 C12N15/29 C12N15/82 C12N15/11 C12N5/10 C07K14/415

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 6 C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	SHEN B. ET AL.: "Partial sequencing and mapping of clones from two maize cDNA libraries" PLANT MOLECULAR BIOLOGY, vol. 26, no. 4, November 1994, pages 1085-1101, XP002042536 see the whole document & "AC T18395" EMBL DATABASE, 23 April 1994, HEIDELBERG, see the whole document ---	10-21, 25,27
X	GRAFI G. ET AL.: "AC U52099" EMBL DATABASE, 26 April 1996, HEIDELBERG, XP002042537 see the whole document ---	10-26
Y	---	1-9,27
	-/-	



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents :

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.
- *Z* document member of the same patent family

Date of the actual completion of the international search

6 October 1997

Date of mailing of the international search report

23.10.97

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Kania, T

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 97/03070

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	QIAN Y ET AL: "BIOLOGICAL FUNCTION OF THE RETINOBLASTOMA PROTEIN REQUIRES DISTINCT DOMAINS FOR HYPERPHOSPHORYLATION AND TRANSCRIPTION FACTOR BINDING" MOLECULAR AND CELLULAR BIOLOGY, vol. 12, no. 12, pages 5363-5372, XP000615356 see the whole document ---	28,29
X	WO 95 06661 A (RES DEV FOUNDATION ;FUNG YUEN KAI (US)) 9 March 1995 * see especially p.31, first par. * ---	28,29
Y	XIE Q. ET AL.: "Identification and analysis of a retinoblastoma binding motif in the replication protein of a plant DNA virus: requirement for efficient viral replication" THE EMBO JOURNAL, vol. 14, no. 16, 15 August 1995, pages 4073-4082, XP002042538 cited in the application * see the whole document, esp. pp. 4079/80 *	1-9,27
A	WO 95 07708 A (UNIV CALIFORNIA ;CANJI INC (US)) 23 March 1995 see the whole document ---	1-29
A	WO 92 05272 A (UNIV CALIFORNIA) 2 April 1992 see the whole document ---	24,26
A	COLLIN S. ET AL.: "The two nonstructural proteins from wheat dwarf virus involved in viral gene expression and replication are retinoblastoma-binding proteins" VIROLOGY, vol. 219, no. 1, 1 May 1996, pages 324-329, XP002042539 * see the whole document, esp. p.325, right col. *	1-29
A	SONI R. ET AL.: "A family of cyclin D homologs from plants differentially controlled by growth regulators and containing the conserved retinoblastoma protein interaction motif" THE PLANT CELL, vol. 7, no. 1, January 1995, pages 85-103, XP002042540 cited in the application * see the whole document, esp. p.97, right col. * --- -/--	1-29

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 97/03070

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
P,X	XIE Q. ET AL.: "Plant cells contain a novel member of the retinoblastoma family of growth regulatory proteins" THE EMBO JOURNAL, vol. 15, no. 18, 16 September 1996, pages 4900-4908, XP002042541 see the whole document ---	1-29
P,X	GRAFI G. ET AL.: "A maize cDNA encoding a member of the retinoblastoma protein family: involvement in endoreduplication" PNAS, U.S.A., vol. 93, no. 17, 20 August 1996, pages 8962-8967, XP002042542 see the whole document -----	1-29

INTERNATIONAL SEARCH REPORT

International application No.

PCT/EP 97/03070

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons.

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☒ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
Please see Further Information sheet enclosed.

3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

INTERNATIONAL SEARCH REPORT

International Application No. PCT/EP 97 03070

FURTHER INFORMATION CONTINUED FROM PCT/ISA210

OBSCURITIES:

Claims 28 and 29 are formulated in a very inconcise manner. Consequently, the subject matter claimed was interpreted as follows and searched :

Claim 28: "A nucleic acid encoding a protein in which one or more sites are altered or deleted, making the protein more resistant to the phosphorylation and thus to it's functionality, for example, linking to E2F or similar "

Claim 29 : Unchanged.

Meaningful search not possible on the basis of all claims:

In claim 18 Seq ID 2 was read as Seq ID 1.

INTERNATIONAL SEARCH REPORT

Information on patent family members

national Application No

PCT/EP 97/03070

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9506661 A	09-03-95	AU 7642694 A	22-03-95
		CA 2170605 A	09-03-95
		CN 1133595 A	16-10-96
		EP 0716660 A	19-06-96
		JP 9502183 T	04-03-97
		ZA 9406595 A	28-02-96

WO 9507708 A	23-03-95	AU 7834994 A	03-04-95
		ZA 9407065 A	03-05-95

WO 9205272 A	02-04-92	CA 2091759 A	18-03-92
		EP 0556231 A	25-08-93
		JP 6501160 T	10-02-94
		US 5324654 A	28-06-94
